

query (SEQ ID NO:1)  
sequence1 (SEQ ID NO:2)  
sequence2 (SEQ ID NO:3)  
sequence3 (SEQ ID NO:4)  
sequence4 (SEQ ID NO:5)  
sequence5 (SEQ ID NO:6)  
sequence6 (SEQ ID NO:7)  
sequence7 (SEQ ID NO:8)

LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSVLTETSVSGDS-VTV  
LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSVLTETSVSGDS-VTV  
LVPFANFG-TVTFTGAEATTSSGTVTAADATLIDIEQNGEVLTSVTVSGST-VTV  
LVQFANFG-TVTFTGASATQNGESVGVTGAQIIDLQQN-SVLTSTVSTSSNS-VTV  
LVNFADFD-TVTFKDCSPSVSG-----STIVDIRQSLEVLTECSTTGTTTVTC  
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC  
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC  
FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC

**FIGURE 1**

>P1;1b4k

structureX:1b4k: 10 :A : 335 :A :

YPYTRLRRNRDDFSRRLVRENVLTVDLILPVFVLDGVNQRESIPSMPGVERLSIDQLLIEAE  
EWVALGIPALALFPVT:PVEKKSLDAAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTH  
GQDGILDDDDGYVLNDVSIIDLVRQALSHAEAGAQQVAPSDMMDGRIGAIRESAG:HTNVRI  
MAYSAKYASAYYGPFRRDAVGSASNLGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGM  
PYLDIVRRVK:DEFRAPTFVYQVSGEYAMHMGAIQNGWLAE:SVILES LTAFKRAGADGILTYF  
AKQAAEQLRR\* (SEQ ID NO:9)

>P1;SC001

sequence:SC001: 13 : : 340 :

EISSVLAGGYNHPLLRRQWQSERQLTKNMLIFPLFISDNPDDEFTEIDSLPNINRIGVNRLKDYLK  
PLVAKGLRSVILFGVPLIPGTKDPVGTAAADDPAGPVIQGIKFIREYFPELYIICDVCLCEYTSH  
GHCGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRGLINANLAHKTFV  
LSYAAKFSGNLYGPFRRDAACSA::PSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPST  
FYLDIMRDASEICKDLPI CAYHVS GEYAMLHAAA EKG VVDLKTIAFESHQGFLRAGARLIITYL  
APEFLDWLDE\* (SEQ ID NO:10)

**FIGURE 17**

>P1;1a28  
structureX: 1a28A : 701 : : 915 : :  
AGHDNTKPDTSSSLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVS  
GQMLYFAPDLILNEQRMKESFYSLCLTMW-QIPQEFVKLQVSQEEFLCMKVLLLLNTI-PLEGLRSQTQFE  
EMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFPPEMMSEVIA  
A\* (SEQ ID NO:11)  
>P1;gi7766906  
sequence: gi7766906 : 27 : : 233 :  
EANMGLNPSSPNPVTNICQAADKQLFTLVEWAKRIPHFSELPLDDQVILLRAGWNELLIASASHRSIA--V  
KDGILLATGLHVHRNSAHSAGVGAI FDRVLTELVS KM RDMQMDKTELGCLRAIVLFNPDS--KGLSNPAEVE  
ALREKVYASLEAYCKHKYP---EQPGRFAKLLRLPALRSIGLKCLEHLFF-FKLIGDT--PIDTFLMEMLE  
A\* (SEQ ID NO:12)

**FIGURE 20**

>P1;1a28  
structureX: 1a28A : 682 : : 921 : :  
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQY  
SWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKE-SSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVL  
LLLN----TIPLEGLR---SQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHL  
YCLNTFIQSRALSVEFPFEMMSEVIAAQLPKIL\* (SEQ ID NO:13)  
sequence: gi3659931 : 14 : : 254 :  
LTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLC  
AWLEILMIGLVWRSMHP--GKLLFAPNLLDRNQKGCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSI  
ILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAGLTLQQQHERLAQLLLILSHIRHMSNKGME  
HLYSMKCKN--VVPLYDLLLEMLD-AHR-LH\* (SEQ ID NO:14)

**FIGURE 24**

>P1;1c3w  
structureX: 1c3wA : 5 : : 231 : :  
TGRPEWIWLALGTALMGLGTLYFLVKMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPPFGGE--  
QN---PIYW-ARYADWLFTTPLLALLDLALLVDADQGTILALVGADGIMIGTGLVGALTKVY--S--YRFVW  
WAISTA-AMLYILYVLFPGF-----SMRPE-VA-STFKVLRNVTVVLSAYPVVWLIGSEG-----AGI---V  
PLNIETLLFMVL-DVSAKVGFGILLRSRAIFG\* (SEQ ID NO:15)  
>P1;1e12A  
sequence: 1e12A : 4 : : 236 : :  
ENALLSSSLWVNVALAGIAILVFVYMGRITIRPGRPRLIWGATLMIPLVSISSYLGLLSGLTVGMIEMPAGHA  
LAGEMVRSQW-GRYLTWALSTPMILLALGLLADVDLGSFTVIAADIGMCTGLAAAMTTS---ALLFRWAF  
YAISCA-FFVVLSALVTDWAASASSAGT--A--EIFDTRLRVLTVVWLGYPIVWAVGV-----EGLALVQ  
SVGATSWAYSVL-DVFAKYVFAFILLRWVANNE\* (SEQ ID NO:16)

FIGURE 27

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>P1;1f88
structureX: 1f88A : 37 : : 308 : :
FSMLAAYMFLLIMLGFPINFLTLYVTQHKKLRT-----PLNYILLNLAVADLFMVFGGFTTTLTSLHGYF
VFGPTGCNLEGFFATLGGEIALWSLVVLAIERVYVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGW
SRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIIPILVIFFCYQQLVFTV-KEAAASATTQKAEKEV
TRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIM* (SEQ ID NO:17)
>P1;1c3wA
sequence: 1c3wA : 2 : : 215 : GRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYA-
ITTLVPAIAFTMYLSMLLGYGLT MVP-FGGEQ
--NPI-YWARYADWLFTTPLL LLDLALLVDA-----D-----QGTILALVGADGIMIGTGLVGAL-----
TKVY-----SY-----RFVWWAISTAAMLYILYVLFFGFMSR--PEV-----ASTFKVL
RNVTVVLWSAYPVVWLIGSEGAGI-----VPLNI--ETLLFMVLDVSAKVGFLILL* (SEQ ID NO:18)

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**FIGURE 29**

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>P1;6prc
structureX: 6prcL : 14 : : 258 : : GTLIGGDLFDFWVGPFVVGFFGVSAIFFIFLGVSLIGYAASQG-P----
---TW-DPFAISINPPDLKYGLG
A-APLLEGGFWQAITVCALGAFISWMLREVEISRKLIGWHVPLAFCVPIFMFCVLQVFRPLLGSWGHAFP
YGILSHLDWVNNFGYQYLNWHYNPGHMSSVSFLFVNAMALGLHGGLILSVANP-GD----GD-----
-KVKTA-EHENQYFRDVVGYSIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRG* (SEQ ID NO:19)
>P1;6prcM
sequence: 6prcM : 34 : : 292 :
YSYWLKIGDAQIGPIYLGASGIAAFAGSTAILIILFNMAAEVHFDPLQFFR--QFFWLGLYPPKAQYGMG
I-PPLHDGGWWLMAGLFMTLSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVP
FGIWPIDWLTAFSIRYGNFYCPWHGFSIGFAYGCGLLFAAHGATILAVARFG-----GDREIEQITDRG
T--AV--ERAALFWRWTIGFNATIESVHRWGWFSLMVMVSASVGILLTGTFVDNW* (SEQ ID NO:20)

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FIGURE 31

>P1;1qj8  
structureX: 1qj8A : 4 : : 148 : :  
TVTGGYAQSDAQGM-NKMGGFNLKYRYEEDNSPLGVIGSFYTE-K--SRTASSGDYN-KNQYYGITAGPA  
YRINDWASIYGVGVGYGKFQTTEYPTYK-NDTSDYGFSYGAGLQFNPMENVALDFSIEQSRIRS-----  
--VDVGTWIAGVGYRF\* (SEQ ID NO:21)  
>P1;1bxwA  
sequence: 1bxwA : 19 : : 171 :  
YHDTGLINNN--GPTHENKLGAGAFGGYQV-NPYVGFEMGYDWL--GRMPYKGSVENGAYKAQGVQLTAKLG  
YPITDDLDIYTRLGGMVWRADTY-SNVYGMNHDGTGSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGT  
RP-DNGMLSLGVSRYF\* (SEQ ID NO:22)

**FIGURE 33**



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>P1;2por
structureX: 2por : 1 : : 301 :
EVKLSGDARMGVMYNGDD---WNFSSRSRVLFMTSGTTDSGLEFGASFKAHESVG-----AETGEDGTV
FLSG-AFGKIEMGDALGASEALFGD--LYEVGYTDLDDRGGNDIPYL-----TGDERLTAEDNPVLLYTY-
SA-----GAFSVAASMS--DGKV-----GETSED-----DAQ---EMAVAAAYT-F--G
NY---TVGLGYEKIDSP-----DTAL-----MADMEQLELAIAKFGATNVKAYYADGELDRDFARAV
FDLTPVAAAAATAVDHKAYGLSVDSTFGATTVGGYVQVLDIDTIDDVTTYGLGASYDLGGGASIVGGIADNDL
PNSDMVADLGVKFKF* (SEQ ID NO:23)
>P1;1osmA
sequence: 1osmA : 10 : : 332 :
KLDLYGKIDGLHYFSDDKDVD-GDQTYMRLGVKGETQINDQLTGYGQWEYNVQ-ANNTESSSDQAWTRLAFA
GLKFGDAGSFDYGRNYGVVY-DVTSWTDVLPE-----FGGDTY-----GSDNFLQSRANGVATYRN-
SDFFGLVDGLNFALQY---QGKNGSVSGEGATNNGRGAL---KQN-----GD---GFGTSVTYD-I--F
D----GISAGFAYANS-----KRTDDQNQLLLGEGDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSL-
-GFANKAQNFEEVAAQYQFDFGLRPSVAYLQSKGKDLNG-YGDQDILKYVDVGATYYFNKNMSTYVDYKINLL
DDNSFTRSAGISTDD* (SEQ ID NO:24)

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**FIGURE 35**

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P1;2mpr
structureX: 2mprA : 2 : : 427 : :
DFHGYARSGIGWTGS-----G---GEQQC-----FQA--TGAQSKYRLGNE-----
--CETYAELKLGQEVWKEGDKSFYFDTNVAYSVNQQND--WEST-DPAFREANVQGKNL---IEWLPGSTIW
AGKRFYQRHD---VHMIDFYWDISGPGAGIENIDLGFGLS-LAATRSTEAGGSYTFSSQNIYDEVKDTAN
DVFDVRLAGLQTNPDGVLELGVYGRANTTDGYKL-ADGASKDGWMFTAHTQSMLKGYNKFVVQYATDAMT
TQKGQARGSDGSSSFTEKINYANKVINNG-NMWRILDHGAISLGDKWDLMYVGMYNIDWDNNL--GTEW
WTVGVPRMPYKWPIMSTLLEVGYDNVKS-QQ-----TGDRNNQYKITLA-QQ---WQAGDSIWSRPAIRI
FATYAKWDEKWKYIKDGNISRYAAAT-NSGISTNSRGDSDEWTFGAQMEIWW* (SEQ ID NO:25)
>P1;1a0tP
sequence: 1a0tP : 4 : : 413 :
EFHGYARSGVIMNDGASTKSGAYITPAGETGG-----AIGRL-----GNQ-----
--ADTYVEMNLEHKQTLNNGATTRFKVMVADGQTSYNDWTASTS-DLNVRQAFVELGNLPTFAGPFKGSTLW
AGKRF--DRDNFDIHWIDSDVFLAGTGGGIYDVKNWDLRSNFSLYGRNFGDIDDSSNSVQNYILTMNHFA
GPLQMMVSGLRKDNDRKDSNG-NLAKGDAANTGV----HALLGLHNDSFYGLRDGSSKTALLYG-HGLG
AEVKGIGSDGA-----LRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQW
ATFNLRLIQAINQNQFALAYEGSYQYMD--LKPEGYNDRQAVNGSFYKLTF--APTFKVGSIQDFFSRPEIRF
YTSWMDWSKKLNNYASDDALGS---DGF-----NSGGEWSFGVQMETWF* (SEQ ID NO:26)

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**FIGURE 37**